confirmations (in order to have a fixed conformation, proteins generally have to be much larger)." Specific binding of a peptide to a target molecule requires the peptide to take up one conformation that is complementary to the binding site. For a decapeptide with three isoenergetic conformations (e.g., β strand, α helix, and reverse turn) at each residue, there are about $6 \cdot 10^4$ possible overall conformations. Assuming these conformations to be equi-probable for the unconstrained decapeptide, if only one of the possible conformations bound to the binding site, then the affinity of the peptide for the target is expected to be about $6 \cdot 10^4$ higher if it could be constrained to that single effective conformation. Thus, the unconstrained decapeptide, relative to a decapeptide constrained to the correct conformation, would be expected to exhibit lower affinity. It would also exhibit lower specificity, since one of the other conformations of the unconstrained decapeptide might be one which bound tightly to a material other than the intended target. By way of corollary, it could have less resistance to degradation by proteases, since it would be more likely to provide a binding site for the protease.--

Please replace the paragraph on page 52, lines 2-14, with the following rewritten paragraph:

--In vitro, disulfide bridges can form spontaneously in polypeptides as a result of air oxidation. Matters are more complicated in vivo. Very few intracellular proteins have disulfide bridges, probably because a strong reducing environment is maintained by the glutathione systems. Disulfide bridges are common in proteins that travel or operate in extracellular spaces, such as snake venoms and other toxins (e.g., conotoxins, charybdotoxin, bacterial entertoxins), peptide hormones, digestive enzymes, complement proteins, immunoglobulins, lysozymes, protease inhibitors (BPTI and its homologues, CMTI-III (Cucurbita maxima trypsin inhibitor III) and its homologues, hirudin, etc.) and milk proteins.--

Please replace the paragraph on page 58, lines 9-26, with the following rewritten paragraph:

--Metal Finger Mini-Proteins. The mini-proteins of the present invention are not limited to those crosslinked by disulfide bonds. Another important class of mini-proteins are analogues of finger proteins. Finger proteins are characterized by finger structures in which a metal ion is coordinated by two Cys and two His residues, forming a tetrahedral arrangement around it. The metal ion is most often zinc(II), but may be iron, copper, cobalt, etc. The "finger" has the consensus sequence (Phe or Tyr)-(1 AA)-Cys-(2-4 Aas)-Cys-(3 Aas)-Phe-(5 Aas)-Leu-(2 Aas)-His-(3 Aas)-His-(5 Aas)(SEQ ID NOs:1,2,3,4,5,6)(BERG88; GIBS88). While finger proteins typically contain many repeats of the finger motif, it is known that a single finger will fold in the presence of zinc ions (FRAN87; PARR88). There is some dispute as to whether two fingers are necessary for binding to DNA. The present invention encompasses mini-proteins with either one or two fingers. It is to be understood that the target need not be a nucleic acid.--

Please replace the paragraph on pages 63-64, lines 31-33 and 1-12, with the following rewritten paragraph:

--Sauer and colleagues (PAKU86, REID88a), and Caruthers and colleagues (EISE85) have shown that some residues on the polypeptide chain are more important than others in determining the 3D structure of a protein. The 3D structure is essentially unaffected by the identity of the amino acids at some loci; at the other loci only one or a few types of amino acid is allowed. In most cases, loci where wide variety is allowed have the amino acids side group directed toward the solvent. Loci where limited variety is allowed frequently have the side group directed toward other parts of the protein. Thus substitutions of amino acids that are exposed to solvent are less likely to affect the 3D structure than are

substitutions at internal loci. (See also SCHU79, p169-171 and CREI84, p239-245, 314-315).--

Please replace the paragraph on page 79, lines 1-6, with the following rewritten paragraph:

--1) SNT which encodes the set [L,P,H,R,V,A,D,G]: a) one acidic (D) and one basic (R), b) both aliphatic (L,V) and aromatic hydrophobics (H), c) large (L,R,H) and small (G,A) side groups, d) rigid (P) and flexible (G) amino acids, e) each amino acid encoded once.--

Please replace the paragraph on page 79, lines 14-17, with the following rewritten paragraph:

--4) VNT which encodes the set [L,P,H,R,I,T,N,S,V,A,D,G]: a) one acidic, one basic, b) all classes: charged, neutral hydrophilic, hydrophobic, rigid and flexible, etc., c) each amino acid encoded once.--

Please replace the paragraph on page 84, lines 1-8, with the following rewritten paragraph:

--We vary a1, c1, g1, a1 and c2 and then calculate t1, g2, and t2. Initially, variation is in steps of 5%. Once an approximately optimum distribution of nucleotides is determined, the region is further explored with steps of 1%. The logic of this program is shown in Table 9. The optimum distribution (the "qfk" codon) is shown in Table 10A and yields DNA molecules encoding each type amino acid with the abundance shown.--

Please replace the paragraph on page 84, lines 9-17, with the following rewritten paragraph:

--Note that this chemistry encodes all twenty amino acids, with acidic and basic amino acids being equiprobable, and the most favored amino acids (serine) is encoded only 2.454 times as often as the least favored amino acid

(tryptophan). The "qfk" vg codon improves sampling most for peptides containing several of the amino acids [F,Y,C,W,H,Q,I,M,N,K,D,E] for which NNK or NNS provide only one codon. Its sampling advantages are most pronounced when the library is relatively small.--

Please replace the paragraph on page 85, lines 4-14, with the following rewritten paragraph:

--If we reduce the prevalence of SER by reducing T_1, C_2, A_1, and G_2, relative to other bases, then we will also reduce the prevalence of PHE, TYR, CYS, PRO, THR, ALA, ARG, GLY, ILE, and ASN. The prevalence of LEU, HIS, VAL, and ASP will rise. If we assume that T_1, C_2, A_1, and G_2 are all lowered to the same extent and that C_1, G_1, T_2, and A_2 are increased by the same amount, we can compute a shift that makes the prevalence of SER equal the prevalences of LEU, HIS, VAL, and ASP. The decreases in each of PHE, TYR, CYS, PRO, THR, ALA, ARG, GLY, ILE, and ASN are not equal; CYS and THR are reduced more than the others.--

Please replace the paragraph on page 89, lines 10-23, with the following rewritten paragraph:

--Several of the preferred simple or complex variegated codons encode a set of amino acids which includes cysteine. This means that some of the encoded binding domains will feature one or more cysteines in addition to the invariant disulfide-bonded cysteines. For example, at each NNT-encoded position, there is a one in sixteen chance of obtaining cystein. If six codons are so varied, the fraction of domains containing additional cysteines is 0.33. Odd numbers of cysteines can lead to complications, see Perry and Wetzel (PERR84, PERR86). On the other hand, many disulfide-containing proteins contain cysteines that do not form disulfides, e.g. trypsin. The possibility of unpaired cysteines can be dealt with in several ways:--

Please replace the paragraph on page 94, lines 17-31, with the following rewritten paragraph:

--In the first round, we assume that the parental protein has no known affinity for the target material. For example, consider the parental mini-protein, similar to that discussed in Example 11, having the structure X_1-C_2-X_3-X_4-X_5-X_6-C_7-X_8 (SEQ ID NO:7) in which C_2 and C_7 form a disulfide bond. Introduction of extra cysteines may cause alternative structures to form which might be disadvantageous. Accidental cysteines at positions 4 or 5 are thought to be potentially more troublesome than at the other positions. We adopt the pattern of variegation: X_1:NNT, X_3:NNT, X_4:NNG, X_5:NNG, X_6:NNT, and X_8:NNT, so that cysteine can not occur at positions 4 and 5 (DNA sequence NNT.TGT.NNT.NNG.NNG.NNT.TGT.NNT has SEQ ID NO:89). (Table 131 shows the number of different amino acids expected in libraries prepared with DNA variegated in this way and comprising different numbers of independent transformants.)--

Please replace the paragraph on page 109, lines 11-30, with the following rewritten paragraph:

--Optionally, DNA encoding a flexible linker of one to 10 amino acids is introduced between the ipbd gene fragment and the Pf3 coat-protein gene. Optionally, DNA encoding the recognition site for a specific protease, such as tissue plasminogen activator or blood clotting Factor Xa, is introduced between the ipbd gene fragment and the Pf3 coat-protein gene. Amino acids that form the recognition sire for a specific protease may also serve the function of a flexible linker. This tripartite gene is introduced into Pf3 so that it does not interfere with expression of any Pf3 genes. To reduce the possibility of genetic recombination, part (3) is designed to have numerous silent mutations relative to the wild-type gene. Once the signal sequence is cleaved off, the IPBD is in the periplasm and the mature coat protein acts as

an anchor and phage-assembly signal. It matters not that this fusion protein comes to rest anchored in the lipid bilayer by a route different from the route followed by the wild-type coat protein.--

Please replace the paragraph on page 138, lines 5-23, with the following rewritten paragraph:

--Consider a mini-protein embedded in LamB. For example, insertion of DNA encoding $G_1NXCX_5XXXCX_{10}SG_{12}$ (SEQ ID NO:8) between codons 153 and 154 of lamB is likely to lead to a wide variety of LamB derivatives being expressed on the suface of E. coli cells. G_1, N_2, S_{11}, and G_{12} are supplied to allow the mini-protein sufficient orientational freedom that is can interact optimally with the target. Using affinity enrichment (involving, for example, FACS via a fluorescently labeled target, perhaps through several rounds of enrichment), we might obtain a strain (named, for example, BEST) that expresses a particular LamB derivative that shows high affinity for the predetermined target. An octapeptide having the sequence of the inserted residues 3 through 10 from BEST is likely to have an affinity and specificity similar to that observed in BEST because the octapeptide has an internal structure that keeps the amino acids in a conformation that is quite similar in the LamB derivative and in the isolated mini-protein.--

Please replace the paragraph on page 155, lines 16-20, with the following rewritten paragraph:

--residue: 17 18 19 20 21 22 23 24 25

5' g|gcc|gcG|GTA|CCG|ATG|CTG|TCT|TTT|GCT|qfk|qfk|-

26 27 28 29 30

|qfk|TTC|TGT|CTC|GAG|cgc|ccg|cga| 3' olig#14--

Please replace the paragraph on page 155, lines 23-27, with the following rewritten paragraph:

--residue : 17 18 19 20 21 22 23 24 25 26
5' g|gcc|gcG|GTA|CCG|ATG|CTG|TCT|TTT|GCT|qfk|qfk|qfk|-
26a 26b 27 28 29 30
|qfk|qfk|TTC|TGT|CTC|GAG|cgc|ccg|cga| 3' olig#14a--

Please replace the paragraph on page 155, lines 30-34, with the following rewritten paragraph:

--residue : 17 18 19 20 21 22 23 24 25 26
5'g|gcc|gcG|GTA|CCG|ATG|CTG|TCT|TTT|GCT|qfk|qfk|qfk|-
26a 26b 26c 26d 27 28 29 30
|qfk|qfk|qfk|qfk|TTC|TGT|CTC|GAG|cgc|ccg|cga| 3'olig#14b--

Please replace the paragraph on pages 155-156, lines 40-44 and 1-6, with the following rewritten paragraph:

--where q is a mixture of (0.26 T, 0.18 C, 0.26 A, and 0.30 G), f is a mixture of (0.22 T, 0.16 C, 0.40 A, and 0.22 G), and k is a mixture of equal parts of T and G. The bases shown in lower case at either end are spacers and are not incorporated into the cloned gene. One of the variegated oligo-nts and the primer are combined in equimolar amounts and annealed. The ds DNA is completed with all four (nt)TPs and Klenow fragment. The resulting dsDNA and RF pLG7 are cut with both KpnI and XhoI, purified, mixed, and ligated. We selected a transformed clone that, when induced with IPTG, binds AHTrp or trp.--

Please replace the paragraph on page 161, lines 2-10, with the following rewritten paragraph:

--The target materials may be organic macromolecules, such as polypeptides, lipids, polynucleic acids, and polusaccharides, but are not so limited. Almost any molecule that is stable in aqueous solvent may be used as a target. The following list of possible targets is given as illustration and not as limitation. The categories are not

strictly mutually exclusive. The omission of any category is not to be construed to imply that said category is unsuitable as a target. Merck Index refers to the Eleventh Edition.--

Please replace the paragraph on page 163, lines 23-25, with the following rewritten paragraph:

--2) ds DNA : 5'-CCGTCGAATCCGC-3' (SEQ ID NO:90)
3'-GGCATTTAGGCG-5' (SEQ ID NO:91)
(Note mismatch)--

Please replace the paragraph on page 163, lines 26-27, with the following rewritten paragraph:

--3) ss DNA : 5'-CGTAACCTCGTCATTA-3'
(No hair pin) (SEQ ID NO:92)--

Please replace the paragraph on page 163, lines 28-30, with the following rewritten paragraph:

--4) ss DNA : 5'-CCGTAGGT
3'-GGCATCCA
(Note hair pin) (SEQ ID NO:93)--

Please replace the paragraph on page 163, lines 31-33, with the following rewritten paragraph:

--5) dsDNA with cohesive ends:
5'-CACGGCTATTACGGT-3' (SEQ ID NO:94)
3'- CCGATAATGCCA-5' (SEQ ID NO:95)--

Please replace the paragraph on page 216, lines 23-25, with the following rewritten paragraph:

--M K K S - rest of VIII
ACT.TCC.TC.ATG.AAA.AAG.TCT. (SEQ ID NOs: 96 and 97)
rest of XI - T S S stop--

Page 216, after line 26, insert the following new paragraph:

(The amino acid sequence MKKS has SEQ ID NO:9).

After paragraph on page 216, line 25, insert the following:

--(The amino-acid sequence MKKS has SEQ ID NO:9.)--

Please replace the paragraph on page 216, lines 29-31, with the following rewritten paragraph:

--(L) K K S - rest of VIII

ACT.TCC.AG.CTG.AAA.AAG.TCT. (SEQ ID NOs: 98 and 99)

rest of XI -T S S stop--

Please replace the paragraph on pages 217-218, lines 25-33 and 1-6, with the following rewritten paragraph:

--With regard to the 'EGGGS linker' (SEQ ID NO:10) extensions of the domain interface, individual phage stocks predicted to contain one or more 5-amino-acid unit extensions were analyzed in a similar fashion. The migration of the extended fusion proteins were readily distinguishable from the parent fusion protein when viewed by western analysis or silver staining. Those clones analyzed in more detail included M13.3X4 (which contains a single inverted EGGGS (SEQ ID NO:10) linker with a predicted amino acid sequence of GSSSL (SEQ ID NO: 16)), M13.3X7 (which contains a correctly oriented linker with a predicted amino acid sequence of EGGGS (SEQ ID NO:10)), M13.3X11 (which contains 3 linkers with an inversion and a predicted amino acid sequence for the extension of EGGGSGSSSLGSSSL (SEQ ID NO:11)) and M13.3Xd which contains an extension consisting of at least 5 linkers or 25 amino acids.--

Please replace the paragraph on page 218, lines 21-31, with the following rewritten paragraph:

--The assay is detailed in Example II, but principally involves the addition of purified anti-BPTI IgG (from the serum of BPTI injected rabbits) to a known titer of phage. Following incubation, protein A-agarose beads are added to bind the IgG and left to incubate overnight. The IgG-protein A beads and any bound phage are removed by centrifugation followed by a retitering of the supernatant to determine any loss of phage. The phage bound to the beads can be acid eluted and titered also. Appropriate controls are included in the assay, such as a wild type phage stock (M13mp18) and IgG purified from normal rabbit pre-immune serum.--

Please replace the paragraph on pages 220-221, lines 30-34 and 1-10, with the following rewritten paragraph:

--To take this analysis one step further, a comparison of phage binding to active and inactivated trypsin is shown in Table 145. The control phage, M13mp18 and BPTI-III MK, demonstrated binding similar to that detailed in Example III. Note that the relative binding is enhanced with trypsin due to the apparent marked reduction in the non-specific binding of the wild type phage to the active protease. M13.3X7 and M13.3X11, which both contain 'EGGGS' linker (SEQ ID NO:10) extensions at the domain interface, bound to anhydrotrypsin and trypsin in a manner similar to BPTI-IIIMK phage. The binding, relative to non-display phage, was approximately 100 fold higher in the anhydrotrypsin binding assay and at least 1000 fold higher in the trypsin binding assay. The binding of another 'EGGGS' linker variant (M13.3Xd) was similar to that of M13.3X7.--

Please replace the paragraph on page 221, lines 11-27, with the following rewritten paragraph:

--To demonstrate the specificity of binding the assays were repeated with human neutrophil elastase (HNE) beads and compared to that seen with trypsin beads Table 146. BPTI has

a very high affinity for trypsin and a low affinity for HNE, hence the BPTI display phage should reflect these affinities when used in binding assays with these beads. The negative and positive controls for trypsin binding were as already described above while an additional positive control for the HNE beads, BPTI(K15L,-MGNG)-III MA (see Example III) was included. The results, shown in Table 146, confirmed this prediction. M13MB48, M13.3X7 and M13.3X11 phage demonstrated good binding to trypsin, relative to wild type phage and the HNE control (BPTI(K15L,MGNG)-III MA) (The amino acid sequence MGNG has SEQ ID NO:12; BPTI(.....,MGNG) denotes a homologue of BPTI having M_{39}, G_{40}, N_{41}, G_{42} where .... may indicate other alterations.), being comparable to BPTI-IIIMK phage. Conversely, poor binding occurred when HNE beads were used, with the exception of the HNE positive control phage.--

Please replace the paragraph on pages 232-233, lines 24-33 and 1-20, with the following rewritten paragraph:

--Fifty µl of BPTI-III MK phage (identified as MK-BPTI is Example II) ($3.7 \cdot 10^{11}$ pfu/ml) in either 50 mM Tris, pH 7.5, 150 mM NaCl, 1.0 mg/ml BSA (TBS/BSA) buffer or 50 mM sodium citrate, pH 6.5, 150 mM NaCl, 1.0 mg/ml BSA (CBS/BSA) buffer were added to 10 µl of a 25% slurry of immobilized trypsin (Pierce Chemical Co., Rockford, IL) also in TBS/BSA or CBS/BSA. As a control, 50 µl MK phage ($9.3 \cdot 10^{12}$ pfu/ml) were added to 10 µl of a 25% slurry of immobilized trypsin in either TBS/BSA or CBS/BSA buffer. The infectivity of BPTI-III MK phage is 25-fold lower than that of MK phage; thus the conditions chosen above ensure that an approximately equivalent number of phage particles are added to the trypsin beads. After 3 hours of mixing on a Labquake shaker (Labindustries Inc., Berkeley, CA) 0.5 ml of either TBS/BSA or CBS/BSA was added where appropriate to the samples. Beads were washed for 5 min and recovered by centrifugation for 30 sec. The supernatant was removed and 0.5 ml of TBS/0.1%

Tween-20 was added. The beads were mixed for 5 minutes on the shaker and recovered by centrifugation as above. The supernatant was removed and the beads were washed an additional five times with TBS/0./1% Tween-20 as described above. Finally, the beads were resuspended in 0.5 ml of elution buffer (0.1 M Hcl containing 1.0 mg/ml BSA adjusted to pH 2.2 with glycine), mixed for 5 minutes and recovered by centrifugation. The supernatant fraction was removed and neutralized by the addition of 130 µ; of 1 M Tris, pH 8.0. Aliquots of the neutrialized elution sample were diluted in LB broth and titered for plaque-forming units on a lawn of cells.--

Please replace the paragraph on page 242, lines 6-27, with the following rewritten paragraph:

--A comparison of the structures of BI-8e and BPTI-(K15L) reveals the presence of three positively charged residues at positions 39, 41, and 42 of BPTI which are absent in BI-8e. These hydrophilic and highly charged residues of BPTI are displayed on a loop which underlies the loop containing the P1 residue and is connected to it <u>via</u> a disulfide bridge. Residues within the underlying loop (in particular residue 39) participate in the interaction of BPTI with the surface of trypsin near the catalytic pocket (BLOW72) and may contribute significantly to the tenacious binding of BPTI to trypsin. However, these hydrophilic residues might hamper the docking of BPTI variants with HNE. In support of this hypothesis, BI-8e displays a high affinity for HNE and contains no charged residues in the region spanning residues 39-42. Hence residues 39 through 42 of wild type BPTI were replaced with the corresponding residues of the human homologue of Bi-8e. We anticipated that a BPTI derivative containing the MET-GLY-ASN-GLY (MGNG) sequence (SEQ ID NO:12) would exhibit a higher affinity for HNE than corresponding derivatives which retain the sequence of wild type BPTI at residues 39-42.--

Please replace the paragraph on pages 242-243, lines 28-34 and 1-19, with the following rewritten paragraph:

--A double stranded oligonucleotide with AccI and EagI compatible ends was designed to introduce the desired alteration of residues 39 to 42 via cassette mutagenesis. Codon 45 was altered to create a new XmnI site, unique in the structure of the BPTI gene, which could be used to screen for mutants. This alteration at codon 45 does not alter the encoded amino-acid sequences. BPTI-IIIMA Rf DNA was digested with AccI. Two oligonucleotides (CYSB and CYST) corresponding to the bottom and top strands of the mutagenic DNA were annealed and ligated to the AccI digested BPTI-III MA Rf DNA. The sample was digested with BglII and the 2.1 kb BglII/EagI fragment was purified. BPTI-III MA Rf was also digested with BglII and EagI and the 6.0 kg fragment was isolated and ligated to the 2.1 kb BglII/EagI fragment described above. Ligation samples were used to transfect competent cells which were plated to permit the formation of plaques on a lawn of cells. Phage derived from plaques were probed with a radioactively labelled oligonucleotide (CYSB) using the Dot Blot Procedure. Positive clones were identified by autoradiography of the Nytran membrane after washing at high stringency conditions. Rf DNA was prepared from Ap^R cultures containing fusion phage which hybridized to the CYSB probe. Restriction enzyme analysis and DNA sequencing confirmed that codons 39-42 of BPTI had been altered. The Rf DNA was designated BPTI(MGNG)-III MA (The amino acid sequence MGNG has SEQ ID NO:12; BPTI(.....,MGNG)-III MA denotes a strain of M13 that displays BPTI(....,MGNG) fused to the gIII protein and that carries the bla gene that confers Ap^r.).--

Please replace the paragraph on pages 250-251, lines 9-35 and 1-5, with the following rewritten paragraph:

--The MYMUT oligonucleotide permits the substitution of 5 hydrophobic residues (PHE, LEU, ILE, VAL, and MET via a DTS

codon (D = approximately equimolar A, T, and G; S = approximately equimolar C and G)) for LYS_{15}. Replacement of LYS_{15} in BPTI with aliphatic hydrophobic residues via semi-synthesis has provided proteins having higher affinity for HNE than BPTI (TANK77, JERI74a,b, WENZ80, TSCH86, BECK88b). At position 16, either GLY or ALA are permitted (GST codon). This is in keeping with the predominance of these two residues at the corresponding positions in a variety of BPTI homologues (CREI87). The variegation scheme at position 17 is identical to that at 15. Limited data is available on the relative contribution of this residue to the interaction of BPTI homologues with HNE. A variety of hydrophobic residues at position 17 was included with the anticipation that they would enhance the docking of a BPTI variant with HNE. Finally at positions 18 and 19, 4 (PHE, SER, THR, and ILE via a WYC codon (W - approximately equimolar A and T; Y = approximately equimolar T and C)) and 5 (SER, PRO, THR, LYS, GLN, and stop via an HMA codon (H = approximately equimolar A, C, and T; M = approximately equimolar A and C)) different amino acids respectively are encoded. These different amino acid residues are found in the corresponding positions of BPTI homologues that are known to bind to HNE (CREI87). Although the amino acids included in the PEPI library were chosen because there was some indication that they might facilitate binding to HNE, it was not and is not possible to predict which combination of these amino acids will lead to high affinity for HNE. The mutagenic oligonucleotide MYMUT was synthesized by Genetic Design Inc. (Houston, Texas).--

Please replace the paragraph on pages 257-258, lines 10-34 and 1-7, with the following rewritten paragraph:

--d) Characterization of Selected Fusion Phage

The pH 2.0 fraction from the third passage of the mini-library was titered and plaques were obtained on a lawn of cells. Twenty plaques were picked at random and phage derived

from plaques were probed with the CYSB oligonucleotide via the Dot Blot Procedure. Autoradiography of the filter revealed that all 20 samples gave a positive hybridization signal indicating that fusion phage were present and the DNA encoding residues 35 to 47 of BPTI(MGNG) is contained within the recombinant M13 genomes. Rd DNA was prepared for the 20 clones and initial dideoxy sequencing revealed that 12 clones were identical. This sequence was designated EpiNEα (SEQ ID NO:45 and SEQ ID NO:108) (Table 207). No DNA sequence changes were observed apart from the planned variegation. Hence the cassette mutagenesis procedure preserved the context of the planned variegation of the pepi gene. The Dot Blot Procedure was employed to probe all 20 selected clones from the pH 2.0 fraction from the third passage of the mini-library with an oligonucleotide homologous to the sequence of EpiNEα. Following high stringency washing, autoradiography revealed that all 20 selected clones were identical in the P1 region. Furthermore dot blot analysis revealed that of the 28 different phage samples pooled to create the mini-library, only one contained the EpiNEα sequence. Hence in just three passes of the mini-library over HNE beads, 1 out of 28 input fusion phage was selected for and appears as a pure population in the lowest pH fraction from the third passage of the library. That the EpiNEα phage elute at pH 3.5 while BPTI(K15V,R17L)-III MA phage elute at a higher pH strongly suggests that the EpiNEα protein has a significantly higher affinity than BPTI(K15V,R17L) for HNE.--

Please replace the paragraph on pages 259-260, lines 25-34 and 1-19, with the following rewritten paragraph:

--b) Characterization of Selected Clones

The pH 2.0 fraction from the third enrichment cycle of MYMUT library was titered on a lawn of cells. Twenty plaques were picked at random. Rf DNA was prepared for each of the clones and fusion phage were collected by PEG precipitation.

Clonnally pure populations of fusion phage in TBS/BSA were prepared and characterized with respect to their affinity for immobilized HNE. pH elution profiles were obtained to determine the stringency of the conditions required to elute bound fusion phage from the HNE matrix. Figure 9 illustrates the pH profiles obtained for EpiNe clones 1 (SEQ ID NO:51), 3 (SEQ ID NO:46) and 7 (SEQ ID NO:48). The pH profiles for all 3 clones exhibit a peak centered on pH 3.5. Unlike the pH profile obtained for the third passage of the MYMUT library, no minor peak centered on pH 4.5 is evident. This is consistent with the clonal purity of the selected EpiNE phage utilized to generate the profiles. The elution peaks are not symmetrical and a prominent trailing edge on the low pH side. In all probability, the 10 minute elution period employed is inadequate to remove bound fusion phage at the low pH conditions. EpiNe clones 1 through 8 have the following characteristics: five clones (identified as EpiNE1 (SEQ ID NO:51), EpiNE3 (SEQ ID NO:46), EpiNE5 (SEQ ID NO:52), EpiNE6 (SEQ ID NO:47), and EpiNE7 (SEQ ID NO:48)) display very similar pH profiles centered on pH 3.5. The remaining 3 clones elute in the pH 3.5 to 4.0 range. There remains some diversity amongst the 20 randomly chosen clones obtained from the pH 2.0 fraction of the third passage of the MYMUT library and these clones might exhibit different affinities for HNE.--

Please replace the paragraph on pages 264-265, lines 32-34 and 1-4, with the following rewritten paragraph:

--Individual phage clones were picked, grown and analyzed for binding to Cat G beads. Figure 13 shows the binding and pH profiles for the individual Cat G binding clones (designated EpiC variants). All clones exhibited minor peaks, superimposed upon a gradual fall in bound phage, at pH elutions of 5 (clones 1 (SEQ ID NOs:54 and 117), 8 (SEQ ID NOs:56 and 119), 10 (SEQ ID NOs:57 and 120) and 11 (SEQ ID NOs: 54 and 117)) or pH 4.5 (clone 7 (SEQ ID NOs:55 and

118)).--

Please replace the paragraph on page 265, lines 5-21, with the following rewritten paragraph:

--DNA sequencing of the EpiC clones, shown in Table 209 (SEQ ID NOs:54 through 58 and 117 through 121), demonstrated that the clones selected for binding to Cat G beads represented a distinct subset of the available sequences in the MYMUT library and a cluster of sequences different from that obtained when enriched with HNE beads. The P1 residue in the EpiC mutants is predominantly MET, with one example of PHE, while in BPTI it is LYS and in the EpiNE variants it is either VAL or LEU. In the EpiC mutants residue 16 is predominantly ALA with one example of GLY and residue 17 is PHE, ILE or LEU. Interestingly residues 16 and 17 appear to pair off by complementary size, at least in this small sample. The small GLY residue pairs with the bulky PHE while the relatively larger ALA residue pairs with the less bulky LEU and ILE. The majority of the available residues in the MYMUT library for positions 18 and 19 are represented in the EpiC variants.--

Please replace the paragraph on page 266, lines 4-14, with the following rewritten paragraph:

--In Example IV, we described engineered protease inhibitors EpiNE1 through EpiNE8 (SEQ ID NOs:46 through 53 and 109-116) that were obtained by affinity selection. Modeling of the structure of the BPTI-Trypsin complex (Brookhaven Protein Data Bank entry 1TPA) indicates that the EpiNE protein surface that interacts with HNE is formed not only by residues 15-19 but also by residues 34-40 that are brought close to this primary loop when the protein folds (HUBE74, HUBE75, OAST88). Acting upon this assumption, we changed amino acid residues in a second loop of the EpiNE7 protein to find EpiNE7 (SEQ ID NO:48) derivatives having higher affinity for HNE.--

Please replace the paragraph on page 267, lines 6-20, with the following rewritten paragraph:

--In the 1TPA complex, ARG_{39} contacts SER_{96}, ASN_{97}, THR_{98}, LEU_{99} (SEQ ID NO:13), GLN_{175}, and TRP_{215}. In HNE, all of the corresponding residues are different! SER_{96} is deleted; ASN_{97} corresponds to ASP_{97} (bearing a negative charge); THR_{98} corresponds to PRO_{98}; LEU_{99} corresponds to the residues VAL_{99}, ASN_{99a}, and LEU_{99b}; GLN_{175} is deleted; and TRP_{215} corresponds to PHE_{215}. Position 39 shows a moderately high degree of variability with 7 different amino acids observed, viz. ARG, GLY, LYS, GLN, ASP, PRO, and MET. Having seen PRO (the most rigid amino acid), GLY (the most flexible amino acid), LYS and ASP (basic and acidic amino acids), we assume that all amino acids are structurally compatible with the aprotinin backbone Because the context of residue 39 has changed so much, we allow all 20 amino acids.--

Please replace the paragraph on page 270, lines 10-31, with the following rewritten paragraph:

--Following this second round of affinity selection, a portion of the beads was mixed with XL1-Blue™ cells and plated to allow plaque formation. Of the resulting plaques, 480 were pooled to form a phage population for a third affinity selection. We repeated the selection procedure described above using a population of phage particles containing $3.0 \cdot 10^9$ plaque forming units. Portions of the pH 2.0 eluate and of the beads were plated with XL1-Blue™ cells to allow formation of plaques. Individual plaques were picked for preparation of RF DNA. From DNA sequencing, we determined the amino acid sequence in the mutated secondary loop of 15 EPINE7-homolog clones. The sequences are given in Table 210 as EPINE7.1 through EPiNE7.20 (SEQ ID Nos:59-70). Three sequences were observed twice: EpiNE7.4 and EpiNE7.14 (SEQ ID NO:63); EpiNE7.8 and EpiNE7.9 (SEQ ID NO:60); and EpiNE7.10 and EpiNE7.20 (SEQ ID NO:65). EpiNE7.4 was eluted at pH 2 while

EpiNE7.14 was obtained by culturing HNE beads that had been washed with pH 2 buffer. Similarly, EpiNE7.10 came from pH 2 elution but EpiNE7.20 came from beads. EpiNE7.8 and EpiNE7.9 both came from pH 2 elution. Interestingly, EpiNE7.8 is found in both the first and second fractionations (EPiNE7.31 (vide infra)).--

Please replace the paragraph on pages 271-272, lines 23-34 and 1-18, with the following rewritten paragraph:

--In a third round of affinity selection, a population of phage particles containing $3.0 \cdot 10^{10}$ plaque forming units was added to 20 µl of 50% slurry of agarose-immobilized HNE beads and incubated for 2 hours at room temperature. We eluted the phage with the following pH washes: pH 7.0, 6.0, 5.0, 4.5, 4.0, 3.5, 3.25, 3.0, 2.75, 2.5, 2.25, and 2.0. After plating a portion of the pH 2.0 eluate fraction for plaque formation, we picked individual plaques for preparation of RF DNA. DNA sequencing yielded the amino acids sequence in the mutated secondary loop for 20 EpiNE7 homolog clones. These sequences, together with EpiNE7 (SEQ ID NO:48), are given in Table 210 as EpiNE7.21 through EpiNE7.40 (SEQ ID NOs:71 through 87). The plaques observed when EpiNEs are plated display a variety of sizes. EpiNE7.21 through EpiNE7.30 (SEQ ID NOs:71 through 80) were picked with attention to plaque size: 7.21, 7.22, and 7.23 from small plaques, 7.24 through 7.30 from plaques of increasing size, with 7.30 coming form a large plaque. TRP occurs at position 39 in EpiNE7.21, 7.22, 7.23, 7.25, and 7.30. Thus plaque size does not correlate with the appearance of TRP at 39. One sequence, EpiNE7.8, from this fractionation is identical to sequence EpiNE7.8 and EpiNE7.9 obtained in the first fractionation. EpiNE7.30, EpiNE7.34, and EpiNE7.35 are identical, indicating that the diversity of the library has been greatly reduced. It is believed that these sequences have an affinity for HNE that is at least comparable to that of EpiNE7 and probably higher. Because the parental EpiNE7

sequence did not recur, it is quite likely that some or all of the EpiNE7-.nn derivatives have higher affinity for HNE than does EpiNE7.--

Please replace the paragraph on page 272, lines 24-31, with the following rewritten paragraph:

--Second, the parental sequence has not recurred. At 39, MET did not occur! At position 34 VAL occurred only once in 35 sequences. At 41, ASN occurred only 4 of 35 times. At 40, GLY occurred 17 of 35 times. At position 36, GLY occurred 34 of 35 times, indicating that ALA is undesirable here. EpiNE7.24 (SEQ ID NO:74) and EpiNE7.36 (SEQ ID NO:83) are most like EpiNE7 (SEQ ID NO:48), having three of the varied residues identical to EpiNE7.--

Please replace the paragraph on pages 273-274, lines 24-34 and 1-28, with the following rewritten paragraph:

--At position 39, all 20 amino acids were allowed, but only seven were seen. TRP is strongly preferred with 19 occurrences, HIS second with six occurrences, and LEU third with 5 occurrences. No homologues of aprotinin have been reported having either TRP or HIS at position 39 as are now disclosed. Although LEU is represented in the NNS codon thrice, TRP and HIS have but one codon each and their prevalence is surprising. We constructed a model having HNE (Brookhaven Protein Data Bank entry 1HNE) and EpiNE7.9 (SEQ ID NO:60) spatially related as in the 1TPA complex. (The α carbons of HNE of conserved internal residues were superimposed on the corresponding α carbons of trypsin, rms deviation $\approx$0.5 Å.) Inspection of this model indicates that TRP_{39} could interact with the loop of HNE that comprises $\underline{VAL}_{99}$, $\underline{ASN}_{99a}$, and $\underline{LEU}_{99b}$. HIS is observed in six cases; HIS is hydrophobic, aromatic, and in some ways similar to TRP. LEU_{39} in EpiNE7.5 could also interact with these residues if the loop moves a short distance. GLU occurred twice while LYS,

ARG, and GLN occurred one each. In BPTI, the C_α of residue 39 is ≈10 Å from the C_α of residue 15 so that TRP_{39} interacts with different features of HNE than do the amino acids substituted at position 15. Residue 34 is well separated from each of the residues 15, 18 and 39; thus is contacts different features on the HNE surface from these residues. Although serine proteases are highly similar near the catalytic site, the similarity diminishes rapidly outside this conserved region. The specificity of serine proteases is in fact determined by more interactions than the P1 residue. To make an inhibitor that is highly specific to HNE, we must go beyond matching the requirement at P1. Thus, the substitutions at 19 (determined in Example IV), 39, 34, and other non-P1 positions are invaluable in customizing the EpiNE to HNE. When making an inhibitor customized to a different serine protease, it is likely that many, if not all, of these positions will be changed to obtain high affinity and specificity. It is a major advantage of the present method that many such derivatives may be tested rapidly.--

Please replace the paragraph on page 275, lines 11-14, with the following rewritten paragraph:

--There has been little if any enrichment at positions 40 and 41. Alanine is somewhat preferred at 40: ALA:GLY::18:17. Both ALA and GLY have been reported in aprotinin homologues.--

Please replace the paragraph on page 275, lines 21-26, with the following rewritten paragraph:

--One sequence, EpiNE7.25 (SEQ ID NO:75) contains an unexpected change at position 47, SER to LEU. Heretofore, all homologues of aprotinin reported have had either SER or THR at position 47. The side groups of SER and THR can form hydrogen bonds to main-chain atoms at the beginning of the short α helix.--

Please replace the paragraph on page 275, lines 27-30, with the following rewritten paragraph:

--The consensus sequence, LYS_{34}, GLY_{36}, TRP_{39}, ALA_{40}, LYS_{41} was not observed. EPiNE7.23 (SEQ ID NO:73) is quite close, differing only at position 40 where the preferences for ALA is very, very weak.--

Please replace the paragraph on pages 275-276, lines 31-33 and 1-9, with the following rewritten paragraph:

--We tested EpiNE7.23 (the sequence closest to consensus) against EpiNE7 (SEQ ID NO:48) on HNE beads. Figure 16 shows the fractionation of strains of phage that display these two EpiNes. Phage that display EpiNE7 are eluted at higher pH than are phage that display EpiNE7.23. Furthermore, more of the EpiNe7.23 phage are retained than of the EpiNe7 phage. Note the peak at pH 2.25 in the EpiNE7.23 elution. This suggests that EpiNE7.23 has a higher affinity for HNE than does EpiNE7. In a similar way, we tested EpiNE7.4 (SEQ ID NO:63) and found that it is not retained on HNE so well as EpiNE7. This is consistent with the fractionation not being complete.--

Please replace the paragraph on page 279, lines 7-14, with the following rewritten paragraph:

--The M13 gene III product contains 'stalk-like' regions as implied by electron micrographic visualization of the bacteriophage (LOPE85). The predicted amino acid sequence of this protein contains repeating motifs, which include:
glu.gly.gly.gly.ser (EGGGS) (SEQ ID NO:10) seven times
gly.gly.gly.ser (GGGS) (SEQ ID NO:14) three times
gly.gly.gly.gly.thr (EGGGT) (SEQ ID NO:15) once.--

Please replace the paragraph on page 279, lines 18-30, with the following rewritten paragraph:

--Two synthetic oligonucleotides were designed and custom

synthesized. GLY is encoded by four codons (GGN); when translated in the opposite direction, these codons give rise to THR, PRO, ALA, and SER. The third base of these codons was picked so that translation of the oligonucleotide in the opposite direction would encode SER. When annealed the synthetic oligonucleotides give the following unit duplex sequence (an EGGGS linker):

```
          E   G   G   G   S (SEQ ID NO:10)
5' C.GAG.GGA.GGA.GGA.TC       3' (SEQ ID NO:100)
3'    TC.CCT.CCT.CCT.AGG.C    5' (SEQ ID NO:101)
     (L) (S) (S) (S) (G) (SEQ ID NO:16)--
```

Please replace the paragraph on pages 279-280, lines 32-35 and 1-6, with the following rewritten paragraph:

--The duplex has a common two base pair 5' overhang (GC) at either end of the linker which allows for both the ligation of multiple units and the ability to clone into the unique NARI recognition sequence present in OCV's M13MB48 and Gem MB42. This site is positioned within 1 codon of the DNA encoding the interface. The cloning of an EGGGS linker (SEQ ID NO:10) (or multiple linker) into the vector NarI site destroys this recognition sequence. Insertion of the EGGGS linker in reverse orientation leads to insertion of GSSSL (SEQ ID NO:16) into the fusion protein.--

Please replace the paragraph on page 280, lines 7-15, with the following rewritten paragraph:

--Addition of a single EGGGS linker at the NarI site of the gene shown in Table 113 leads to the following gene:

```
79  80  80a 80b 80c 80d 80e 81  82  83  84
 G   G   E   G   G   G   S   A   A   E   G   (SEQ ID NO:17)
          ----------------
GGT.GGC.GAG.GGA.GGA.GGA.TCC.GCC.GCT.GAA.GGT (SEQ ID NO:102)
       ------------------                    --
```

Please replace the paragraph on page 281, lines 31-32, with the following rewritten paragraph:

--M13.3X4 (GG)C.GGA.TCC.TCC.TCC.CT(C.GCC) (SEQ ID NO:103)
gly ser ser ser leu (AA 6-10 of SEQ ID NO:11)--

Please replace the paragraph on page 281, lines 34-35, with the following rewritten paragraph:

--M13.3X7 (G C.GAG.GGA.GGA.GGA.TC(C.GCC) (SEQ ID NO:104)
glu gly gly gly ser (SEQ ID NO: 10)--

Please replace the paragraph on pages 281-282, line 37 and lines 1-5, with the following rewritten paragraph:

--M13.3X11 (GG)C.GAG.GGA.GGA.GGA.TCC.GGA.TCC.TCC.
glu gly gly gly ser gly ser ser

TCC.CTC.GGA.TCC.TCC.TCC.CT(C.GCCC)(SEQ ID NO:105)
ser leu gly ser ser ser leu (SEQ ID NO:18)--

Please replace the paragraph on page 316, line 1, with the following rewritten paragraph:

--X_1-X_2-C-X_3-X_4-X_5-X_6-C-X_7-X_8 (SEQ ID NO:19)--

Please replace the paragraph on page 319, lines 22-24, with the following rewritten paragraph:

--Mini-proteins with two disulfide bonds may be modelled after the α-conotoxins, e.g., GI, GIA, GII, MI, and SI. These have the following conserved structure (SEQ ID NOs:20-31):--

After the table on page 321, line 29, please insert:

--(RVT.VYT.RRS.VHG.VHG.RMG has SEQ ID NO:106).--

Please replace the paragraph on page 322, line 32 to page 323, line 5 with the following rewritten paragraph:

--The cone snails (Conus) produce venoms (conotoxins) which are 10-30 amino acids in length and exceptionally rich in disulfide bonds. They are therefore archetypal mini-

proteins. Novel mini-proteins with three disulfide bonds may be modelled after the μ-(GIIIA, GIIIB, BIIIC) or Ω-(GVIA, GVIC, GVIIA, GVIIB, MVIIA, MVIIB, etc.) conotoxins. The μ-conotoxins have the following conserved structure (SEQ ID NO:32):--

Please replace the paragraph on page 323, lines 13-16 with the following rewritten paragraph:

--No 3D structure of a μ-conotoxin has been published. Hidaka et al. (HIDA90) have established the connectivity of the disulfides. The following diagram depicts geographutoxin I (also known as μ-conotoxin GIIIA), whose sequence is SEQ ID NO:33.--

Please replace the paragraph on page 324, line 3, with the following rewritten paragraph:

--The Ω-conotoxins may be represented as follows (SEQ ID NO:34 through 39):--

After the table on page 325, line 33, please insert the following:

--(VYT.VNT.NNK.VWG has SEQ ID NO:107).--

Please replace the paragraph on page 327, lines 4-9, with the following rewritten paragraph:

--Sequences such as
HIS-ASN-GLY-MET-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-HIS-ASN-GLY-CYS (SEQ ID NO:40)
and
CYS-ASN-GLY-MET-Xaa-Xaa-Xaa-Xaa-Xaa-Xaa-HIS-ASN-GLY-HIS (SEQ ID NO:41)
are likely to combine with Cu(II) to form structures as shown in the diagram:--

Please replace the paragraph on page 327, line 38 with

the following rewritten paragraph:

--For example (SEQ ID NO: 42),--

Please replace the paragraph on pages 329-330, lines 32-33 and 1-2, with the following rewritten paragraph:

--One preferred example of a CYS::zinc cross linked mini-protein comprises residues 440 to 461 of the sequence shown in Figure 1 of HARD90. The residues 444 through 456 (SEQ ID NO:43) may be variegated. One such variegation is as follows:--

Please replace the paragraph on page 340, lines 4-9, with the following rewritten paragraph:

--A. Optimized qfk Codon, Restrained by [D]+[E] = [K]+[R]

	T	C	A	G	
1	.26	.18	.26	.30	q
2	.22	.16	.40	.22	f
3	.5	.0	.0	.5	k--

Please replace the paragraph on page 349, the first line after the table, with the following rewritten paragraph:

--1 BPTI (SEQ ID NO:44)--

Page 446, after the last line, please insert the following:

--(The amino acids referred to in Table 130 need not be in sequence, but if they are, the sequences all have SEQ ID NO:88).--

Page 450, after the last line, please insert the following:

--(The amino acids referred to in Table 131 need not be in sequence, but if they are, the sequences all have SEQ ID NO:88).--

Please replace the paragraph on page 458, lines 1-2, with the following rewritten paragraph:

--Table 160: pH Profile of BPTI-III MK phage and EpiNE1 phage binding to Cat G beads.--

Please replace the paragraph on page 458, line 4, with the following rewritten paragraph:

--BPTI-IIIMK (BPTI has SEQ ID NO:44)--

Please replace the paragraph on page 458, line 17, with the following rewritten paragraph:

--EpiNE1 (EpiNE1 has SEQ ID NO:51)--

Page 465, after line 11, insert the following new paragraph:

(SEQ ID NO:45).

Please also insert enclosed substitute pages 466, 466a, and 467-471, replacing original pages 466-471. These pages have been amended solely to provide the required sequence ID numbers.

TABLE 208
SEQUENCES OF THE EpiNE CLONES IN THE P1 REGION

CLONE IDENTIFIERS	SEQUENCE
EpiNE3 (amino-acid: SEQ ID NO:46)	1 1 1 1 1 1 1 2 2 3 4 5 6 7 8 9 0 1
3, 9, 16, 17, 18, 19	P C V G F F S R Y CCT.TGC.GTC.GGT.TTC.TTC.TCA.CGC.TAT (DNA: SEQ ID NO:109)
EpiNE6 (amino-acid: SEQ ID NO:47)	1 1 1 1 1 1 1 2 2 3 4 5 6 7 8 9 0 1
6	P C V G F F Q R Y CCT.TGC.GTC.GGT.TTC.TTC.CAA.CGC.TAT (DNA: SEQ ID NO:110)
EpiNE7 (amino-acid: SEQ ID NO:48)	1 1 1 1 1 1 1 2 2 3 4 5 6 7 8 9 0 1
7, 13, 14, 15, 20	P C V A M F P R Y CCT.TGC.GTC.GCT.ATG.TTC.CCA.CGC.TAT (DNA: SEQ ID NO:111)
EpiNE4 (amino-acid: SEQ ID NO:49)	1 1 1 1 1 1 1 2 2 3 4 5 6 7 8 9 0 1
4	P C V A I F P R Y CCT.TGC.GTC.GCT.ATC.TTC.CCA.CGC.TAT (DNA: SEQ ID NO:112)

TABLE 208
SEQUENCES OF THE EpiNE CLONES IN THE P1 REGION
(continued)

CLONE IDENTIFIERS	SEQUENCE
EpiNE8 (amino-acid: SEQ ID NO:50)	
	1 1 1 1 1 1 1 2 2
	3 4 5 6 7 8 9 0 1
8	P C V A I F K R S
	CCT.TGC.GTC.GCT.ATC.TTC.AAA.CGC.TCT
	(DNA: SEQ ID NO:113)
EpiNE1 (amino-acid: SEQ ID NO:51)	
	1 1 1 1 1 1 1 2 2
	3 4 5 6 7 8 9 0 1
1, 10	P C I A F F P R Y
11, 12	CCT.TGC.ATC.GCT.TTC.TTC.CCA.CGC.TAT
	(DNA: SEQ ID NO:114)
EpiNE5 (amino-acid: SEQ ID NO:52)	
	1 1 1 1 1 1 1 2 2
	3 4 5 6 7 8 9 0 1
5	P C I A F F Q R Y
	CCT.TGC.ATC.GCT.TTC.TTC.CAA.CGC.TAT
	(DNA: SEQ ID NO:115)
EpiNE2 (amin-acid: SEQ ID NO:53)	
	1 1 1 1 1 1 1 2 2
	3 4 5 6 7 8 9 0 1
2	P C I A L F K R Y
	CCT.TGC.ATC.GCT.TTG.TTC.AAA.CGC.TAT
	(DNA: SEQ ID NO:116)

Table 209: DNA sequences and predicted amino acid sequences around the P1 region of BPTI analogues selected for binding to Cathepsin G.

Clone	P1 15	16	17	18	19	
BPTI	AAA .	GCG .	CGC .	ATC .	ATC	
(SEQ ID NO:44)	LYS	ALA	ARG	ILE	ILE	
EpiC 1 (a)	ATG .	GGT .	TTC .	TCC .	AAA	SEQ ID NO:117
(SEQ ID NO:54)	MET	GLY	PHE	SER	LYS	
EpiC 7	ATG .	GCT .	TTG .	TTC .	AAA	SEQ ID NO:118
(SEQ ID NO:55)	MET	ALA	LEU	PHE	LYS	
EpiC 8 (b)	TTC .	GCT .	ATC .	ACC .	CCA	SEQ ID NO:119
(SEQ ID NO:56)	PHE	ALA	ILE	THR	PRO	
EpiC 10	ATG .	GCT .	TTG .	TTC .	CAA	SEQ ID NO:120
(SEQ ID NO:57)	MET	ALA	LEU	PHE	GLN	
EpiC 20	ATG .	GCT .	ATC .	TCC .	CCA	SEQ ID NO:121
(SEQ ID NO:58)	MET	ALA	ILE	SER	PRO	

(a) Clones 11 and 31 also had the identical sequence.

(b) Clone 8 also contained the mutation Tyr 10 to ASN.

Table 210
Derivatives of EpiNE7 (SEQ ID NO:48) Obtained
by Variegation at positions 34, 36, 39, 40 and 41

EpiNE7 (SEQ ID NO:48)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFVYGGCmgngNNFKSAEDCMRTCGGA
1 2 3 4 5
12345678901234567890123456789012345678901234567890123456789012345678

EpiNE7.6 (SEQ ID NO:59)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFlYgGCkgkGNNFKSAEDCMRTCGGA

EpiNE7.8, EpiNE7.9, and EpiNE7.31 (SEQ ID NO:60)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFeYgGCwakGNNFKSAEDCMRTCGGA

EpiNE7.11 (SEQ ID NO:61)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFgYaGCrakGNNFKSAEDCMRTCGGA

EpiNE7.7 (SEQ ID NO:62)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFeYgGChaeGNNFKSAEDCMRTCGGA

EpiNE7.4 and EpiNE7.14 (SEQ ID NO:63)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFlYgGCwaqGNNFKSAEDCMRTCGGA

EpiNE7.5 (SEQ ID NO:64)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFrYgGClaeGNNFKSAEDCMRTCGGA

EpiNE7.10 and EpiNE7.20 (SEQ ID NO:65)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFdYgGChadGNNFKSAEDCMRTCGGA

EpiNE7.1 (SEQ ID NO:66)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFkYgGClahGNNFKSAEDCMRTCGGA

EpiNE7.16 (SEQ ID NO:67)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFtYgGCwanGNNFKSAEDCMRTCGGA

EpiNE7.19 (SEQ ID NO:68)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFnYgGCegkGNNFKSAEDCMRTCGGA

EpiNE7.12 (SEQ ID NO:69)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFqYgGCegyGNNFKSAEDCMRTCGGA

EpiNE7.17 (SEQ ID NO:70)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFqYgGClgeGNNFKSAEDCMRTCGGA

EpiNE7.21 (SEQ ID NO:71)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFhYgGCwgqGNNFKSAEDCMRTCGGA

Table 210: Derivatives of EpiNE7 (SEQ ID NO:48) Obtained by Variegation at positions 34, 36, 39, 40 and 41 (continued)

```
                ♦♦♦♦♦                          ****
EpiNE7 (SEQ ID NO:48)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFVYGGCmgngNNFKSAEDCMRTCGGA
         1         2         3         4         5
12345678901234567890123456789012345678901234567890123456789

                ↓↓↓↓↓                  ♦  ♦  ♦♦♦↓
EpiNE7.22 (SEQ ID NO:72)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFhYgGCwgeGNNFKSAEDCMRTCGGA

EpiNE7.23 (SEQ ID NO:73)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFkYgGCwgkGNNFKSAEDCMRTCGGA

EpiNE7.24 (SEQ ID NO:74)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFkYgGChgnGNNFKSAEDCMRTCGGA

EpiNE7.25 (SEQ ID NO:75)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFpYgGCwakGNNFKlAEDCMRTCGGA

EpiNE7.26 (SEQ ID NO:76)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFkYgGCwghGNNFKSAEDCMRTCGGA

EpiNE7.27 (SEQ ID NO:77)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFnYgGCwgkGNNFKSAEDCMRTCGGA

EpiNE7.28 (SEQ ID NO:78)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFtYgGClghGNNFKSAEDCMRTCGGA

EpiNE7.29 (SEQ ID NO:79)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFtYgGClgyGNNFKSAEDCMRTCGGA

EpiNE7.30, EpiNE7.34, and EpiNE7.35 (SEQ ID NO:80)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFkYgGCwaeGNNFKSAEDCMRTCGGA

EpiNE7.32 (SEQ ID NO:81)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFgYgGCwgeGNNFKSAEDCMRTCGGA

EpiNE7.33 (SEQ ID NO:82)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFeYgGCwanGNNFKSAEDCMRTCGGA

EpiNE7.36 (SEQ ID NO:83)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFvYgGChgdGNNFKSAEDCMRTCGGA

EpiNE7.37 (SEQ ID NO:84)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFmYgGCqgkGNNFKSAEDCMRTCGGA

EpiNE7.38 (SEQ ID NO:85)
RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFyYgGCwakGNNFKSAEDCMRTCGGA
```

Table 210 (continued)
Derivatives of EpiNE7 (SEQ ID NO:48) Obtained by Variegation at positions 34, 36, 39, 40 and 41

```
5
 EpiNE7  (SEQ ID NO:48)                          ****
                 ♦♦♦♦♦
 RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFVYGGCmgngNNFKSAEDCMRTCGGA
                  1         2         3         4         5
10123456789012345678901234567890123456789012345678901234567
                                                 ♦ ♦  ♦♦♦↓
                 ↓↓↓↓↓
 EpiNE7.39  (SEQ ID NO:86)
15RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFmYgGCwgdGNNFKSAEDCMRTCGGA

 EpiNE7.40  (SEQ ID NO:87)
 RPDFCLEPPYTGPCvAmfpRYFYNAKAGLCQTFtYgGChgnGNNFKSAEDCMRTCGGA
```

Table 210: Derivatives of EpiNE7 Obtained by Variegation at positions 34, 36, 39, 40 and 41 (continued)

Notes:

a) ♦ indicates variegated residue. * indicates imposed change. ↓ indicates carry over from EpiNE7.

b) The sequence M_{39}-GNG in EpiNE7 (indicated by *) was imposed to increase similarity to ITI-D1.

b) Lower case letters in EpiNE7.6 to 7.38 indicate changes from BPTI, that were selected in the first round (residues 15-19) or positions where the PBD was variegated in the second round (residues 34, 36, 39, 40, and 41).

c) All EpiNE7 derivatives have G_{42}.